

SEQUENCE LISTING



<110> Quertermous, Thomas
 Hogan, Brigid
 Snodgrass, Ralph H
 Zupancic, Thomas J

<120> Antibodies Binding to Polypeptides Encoded by Developmentally-
 Regulated Endothelial Cell Locus-1

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<140> US 09/237,981
 <141> 1999-01-25

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<170> PatentIn version 3.1

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Xaa Ala Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu
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Ala Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys
35 40 45

Gln Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His
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Arg Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile
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35 40 45

Thr Gly Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His
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Ser Met Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His
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Ser Ser Ser Gln Asp Gly His His Trp Thr Xaa Xaa Gln Ile Leu Tyr
35 40 45

Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro
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35 40 45

Asp Asn Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val
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35 40 45

Lys Asn Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro
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Arg Tyr Ser Leu Asp Asn Val Ser Trp Phe Xaa Xaa Xaa Xaa Xaa Glu
 35 40 45

Tyr Arg Asp Gly Ala Ala Ile Thr Gly Val Thr Asp Arg Asn Thr Val
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Val Asn His Phe Phe Asp Thr Pro Ile Arg Ala Arg Ser Ile Ala Ile
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His Pro Leu Thr Xaa
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 20 25 30

Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
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Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
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Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn	
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ccg aac ccc tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat	747
Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp	
30 35 40	
gat tcc ttt tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc	795
Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys	
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Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala	
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ggt ccc tgc atc cct aac cca tgc cat aac gga gga acc tgt gag ata	891
Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile	
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agc gaa gcc tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt	939

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Pro	Arg	Gly	Phe	Asn	Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys		
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gaa	gct	gag	cct	tgc	aga	aat	ggc	gga	ata	tgt	acc	gac	ctt	gtt	gct		1035
Glu	Ala	Glu	Pro	Cys	Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala		
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Asn	Tyr	Ser	Cys	Glu	Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln		
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Tyr	Lys	Cys	Ser	Gly	His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn		
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cag	caa	atc	aca	gct	tca	tct	aat	cac	cga	gct	ctt	ttt	gga	ctc	cag		1179
Gln	Gln	Ile	Thr	Ala	Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln		
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Lys	Trp	Tyr	Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn		
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gcc	tgg	aca	gct	gct	gaa	aat	gac	aga	tgg	cca	tgg	att	cag	ata	aat		1275
Ala	Trp	Thr	Ala	Ala	Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Ile	Asn		
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Leu	Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys		
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agg	att	gga	agc	cca	gag	tac	ata	aaa	tcc	tac	aaa	att	gcc	tac	agc		1371
Arg	Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Ser	Tyr	Lys	Ile	Ala	Tyr	Ser		
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Asn	Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu		
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Leu	Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	
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Asp	Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Val	Phe	Arg	Thr	Leu	Asn	Met	Asp	
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Arg	Lys	Asp	Lys	Val	Phe	Gln	Gly	Asn	Phe	Asp	Asn	Asp	Thr	His	Arg	
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Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
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Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
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Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
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Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys

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<400> 11

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<400> 13

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 1 5

<210> 14
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 14

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Val	Pro	Gln	Phe	Gly	Lys	Gly	Asp	Ile	Cys	Asp	Pro	Asn	Pro	Cys	Glu
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Asn	Gly	Gly	Ile	Cys	Leu	Pro	Gly	Leu	Ala	Val	Gly	Ser	Phe	Ser	Cys
65						70					75				80
Glu	Cys	Pro	Asp	Gly	Phe	Thr	Asp	Pro	Asn	Cys	Ser	Ser	Val	Val	Glu
				85					90					95	
Val	Ala	Ser	Asp	Glu	Glu	Glu	Pro	Thr	Ser	Ala	Gly	Pro	Cys	Thr	Pro
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Lys	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu
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210					215					220					
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225					230					235					240
Glu	Asn	Asp	Arg	Trp	Lys	Arg	Trp	Ile	Gln	Ile	Asn	Leu	Gln	Arg	Lys
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			260					265					270		
Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	Asp	Gly	Lys
		275					280					285			
Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp	Met	Val	Phe
	290					295					300				
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305					310					315					320
Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Val	Cys	Arg	Arg
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His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu	Ser	Gly	Cys
			340					345					350		
Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp	Tyr	Gln	Ile
		355					360					365			
Thr	Ala	Ser	Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met	Phe	Thr	Trp
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385					390					395					400
Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	Val	Asp	Leu	Leu

405

410

415

Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe
 420 425 430

Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
 435 440 445

Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys
 450 455 460

Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
 465 470 475 480

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
 485 490 495

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
 500 505 510

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<210> 15
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 15

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Ser Met Glu

<210> 16
 <211> 9

<212> PRT
 <213> Homo sapiens

<400> 16

Glu Thr Glu Trp Phe Phe Phe Phe Ser
 1 5

<210> 17
 <211> 9
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<400> 17

Lys Ser Gly Gln Ile Met Val Gly Asn
 1 5

<210> 18
 <211> 4
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<400> 18

Arg Cys Phe Tyr
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<210> 19
 <211> 318
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 <213> mouse

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tttcgtggaa atgttgataa caacacacca tatgctaatt ctttcacacc cccaatcaaa	240
gctcagtatg taagactcta cccccaaatt tgtcgaaggc attgtacttt aagaatggaa	300
cttcttggct gtgagctc	318

85

90

95

Asp Gly Xaa Arg Lys Phe Glu Phe Ile Gln Asp Glu Ser Gly Gly Asp
 100 105 110

Lys Glu Phe Leu Gly Asn Leu Asp Asn Asn Ser Leu Lys Val Asn Met
 115 120 125

Phe Asn Pro Thr Leu Glu Ala Gln Tyr Ile Arg Leu Tyr Pro Val Ser
 130 135 140

Cys His Arg Gly Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu Leu
 145 150 155 160

His Gly Cys Leu Glu Pro Leu Gly Leu Lys Asn Asn Thr Ile Pro Asp
 165 170 175

Ser Gln Met Ser Ala Ser Ser Ser Tyr Lys Thr Trp Asn Leu Arg Ala
 180 185 190

Phe Gly Trp Tyr Pro His Leu Gly Arg Leu Asp Asn Gln Gly Leu Ile
 195 200 205

Asn Ala Trp Thr Ala Gln Ser Asn Ser Ala Lys Glu Trp Leu Gln Val
 210 215 220

Asp Leu Gly Thr Gln Arg Gln Val Thr Gly Ile Ile Thr Gln Gly Ala
 225 230 235 240

Arg Asp Phe Gly His Ile Gln Tyr Val Glu Ser Tyr Lys Val Ala His
 245 250 255

Ser Asp Asp Gly Val Gln Trp Thr Val Tyr Xaa Xaa Glu Glu Gln Gly
 260 265 270

Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys

275

280

285

Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro
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Val Ser Trp His Asn Arg Ile Thr Leu Arg Leu Glu Leu Leu Gly Cys
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Tyr	Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp
		35					40					45			
Thr	Ala	Ala	Glu	Asn	Asp	Arg	Trp	Asn	Arg	Trp	Ile	Gln	Ile	Asn	Leu
	50					55					60				
Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg
65					70					75					80
Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn
				85					90					95	
Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp
			100					105					110		
Met	Val	Phe	Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser
		115					120					125			
Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Val
	130					135					140				
Cys	Arg	Arg	His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu
145					150					155					160
Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp
				165					170					175	
Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met
			180					185					190		
Phe	Thr	Trp	Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	Val
		195					200					205			
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<220>
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<400> 20

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 1 5 10 15

Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp
 20 25 30

Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp
 35 40 45

His Ala Ser Asn Tyr Asp Xaa Ser Lys Pro Trp Ile Gln Val Asn Leu
 50 55 60

Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg
 65 70 75 80

Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu

Xaa Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala
 225 230 235 240

Lys Asp Xaa Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr
 245 250 255

Ser Asn Asp Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg
 260 265 270

Lys Asp Lys Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
 275 280 285

Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro
 290 295 300

Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys
 305 310 315 320

Thr

<210> 22
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 22

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
 1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile
 20 25

<210> 23
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<213> Homo sapiens

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<222> (20)..(24)

<223> Placeholder used in the sequence comparison of SEQ.ID.NOS.23-26

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1 5 10 15

Ala Val Gly Xaa Xaa Xaa Xaa Xaa Ser Phe Ser Cys Glu Cys Pro Asp
20 25 30

Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp
35 40 45

Glu Glu Glu Pro Thr Ser Ala Gly Pro
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<210> 24

<211> 43

<212> PRT

<213> Homo sapiens

<400> 24

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1 5 10 15

Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
20 25 30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
35 40

<210> 25

<211> 42

<212> PRT

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<222> (18)..(24)

<223> Placeholder used in the sequence comparison of SEQ.ID.NOS.23-26

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Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Tyr	Ser	Cys	Glu	Cys	Pro	Gly
			20						25					30		

Glu	Phe	Met	Gly	Arg	Asn	Cys	Glu	Tyr	Lys
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<211> 40

<212> PRT

<213> Artificial sequence

<220>

<223> consensus EGF-like domain amino acid sequence

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<222> (2)..(4)

<223> nonconsensus sequence

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<222> (7)..(7)

<223> nonconsensus sequence

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> nonconsensus sequence

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 <222> (13)..(25)
 <223> nonconsensus sequence

<220>
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 <222> (29)..(29)
 <223> nonconsensus sequence

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 <222> (40)..(40)
 <223> nonconsensus sequence

<400> 26

Cys	Xaa	Xaa	Xaa	Pro	Cys	Xaa	Asn	Gly	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Xaa
1				5				10						15	

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
 20 25 30

Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
 35 40

<210> 27
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 <223> unknown sequence

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 gaagcatacc gaggggatac attcataggc tatgtttgta aatgtccccg aggatttaat 240
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 atatgtacag 310

<210> 28
 <211> 2308
 <212> DNA
 <213> mouse

<220>
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 <222> (550)..(1212)
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<220>
 <221> misc_feature
 <222> (1819)..(1821)
 <223> unknown sequence

<400> 28

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cgcgcctcgc ctactgtgcc ctccgctacg accccggacc agcccaggtc acgtccgtga      540
gaagggatc atg aag cac ttg gta gca gcc tgg ctt ttg gtt gga ctc agc      591
      Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser
            1             5             10

ctc ggg gtg ccc cag ttc ggc aaa ggt gac att tgc aac ccg aac ccc      639
Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro
15             20             25             30

tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat gat tcc ttt      687
Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe
            35             40             45

tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc tct agt gtt      735
Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val
            50             55             60

gtg gag gtt gca tca gat gaa gaa aag cct act tca gca ggt ccc tgc      783
Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys
            65             70             75

atc cct aac cca tgc cat aac gga gga acc tgt gag ata agc gaa gcc      831
Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala
            80             85             90

tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt cct cgg gga      879
Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly
95             100             105             110

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Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser	
130 135 140	
tgt gaa tgc cca gga gaa ttt atg gga cga aat tgt caa tat aaa tgc	1023
Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys	
145 150 155	
tct ggg cac ttg gga atc gaa ggt ggg atc ata tct aat cag caa atc	1071
Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile	
160 165 170	
aca gct tca tct aat cac cga gct ctt ttt gga ctc cag aag tgg tat	1119
Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr	
175 180 185 190	
ccc tac tat gct aga ctt aat aag aag ggc ctt ata aat gcc tgg aca	1167
Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr	
195 200 205	
gct gct gaa aat gac aga tgg cca tgg att cag gta aca gtg gga	1212
Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly	
210 215 220	
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aattcatagt gccttatatc ctcacagcc atctgacttt actacagaag aaaacaatga	1752
aatgatgcat taagtgcttt gctagaagaa acatcatagc aaagctgata gccacattc	1812

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tgtgcannna agcttccaga gcactcgaga aaaagcagaa atgagatggt ttatgaaaac 1872
cgaaaagata atctgatttc tgtgaaatat actttttgatc atgtgggttct ttaagatagt 1932
cactaacaag tcattagtag cagataccaa atgggagaaa atttccagta tactgagggt 1992
caaggcagtc atgctgaaac tacatgaggt caggaaagtt ttgaaataag gtgatttttg 2052
aaggatacct tcaactggcc tagattttca agaaacagtg taatcaacag ccaaacaatga 2112
gaatctagct aacagcattt agaaaaccag aactaagagt gttactgggg aattgcattt 2172
aaatccagta tgagagtttg caaatgccgt attcttctaa ggggtttgtg ccacattttg 2232
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ataaaagccg gaattc 2308

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<210> 29
<211> 221
<212> PRT
<213> mouse

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<220>
<221> misc_feature
<222> (1819)..(1821)
<223> unknown sequence

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<400> 29

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Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
1           5           10           15

```

```

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
          20           25           30

```

```

Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
          35           40           45

```

```

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50           55           60

```

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
115 120 125

Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
130 135 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145 150 155 160

His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165 170 175

Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
195 200 205

Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly
210 215 220

<210> 30

<211> 481

<212> PRT

<213> Homo sapiens

<400> 30

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly

1

5

10

15

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
 20 25 30

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
 35 40 45

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
 50 55 60

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
 65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
 85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
 100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
 115 120 125

Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
 130 135 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
 145 150 155 160

Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
 165 170 175

Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
 180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala

195

200

205

Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys
 210 215 220

Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser
 225 230 235 240

Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys
 245 250 255

Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe
 260 265 270

Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro
 275 280 285

Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg
 290 295 300

His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys
 305 310 315 320

Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
 325 330 335

Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp
 340 345 350

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
 355 360 365

Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu
 370 375 380

Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe

400

Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Gly Pro Cys Thr Pro
35 40 45

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
50 55 60

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
65 70 75 80

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
85 90 95

Lys Asn Gly Gly Ile Cys Thr
100

INS
01